

Figure 1a / 3**SEQ ID NO:1**

1 MILSLLFSLG GPLGWGLLGA WAQASSTSLS DLQSSRTPGV WKAEEADTGK DPVGRNWCPY
 61 PMSKLVTLLA LCKTEKFLLI SQQPCPQGAP DCQKVVKMYR MAHKPVYQVK QKVLTSLAWR
 121 CCPGYTGPNC EHHDSMAIPE PADPGDSHQE PQDGPVSFKP GHЛАAVINEV EVQQEQQEHL
 181 LGDLQNDVHR VADSLPGLWK ALPGNLTAAS LSNDVKNVGR CCEAEAGAGA ASLNASLHGL
 241 HNALFATQRS LEQHQRLFHS LFGNFQGLME ANVSLDLGKL QTMLSRKGKK QQKDLLEAPRK
 301 RDKKEAEPLV DIRVTGPVPG ALGAALWEAG SPVAFYASFS EGTAALQTVK FNTTYINIGS
 361 SYFPEHGYFR APERGVYLFA VSVEFGPGPG TGQLVFGHH RTPVCTTGQG SGSTATVFAM
 421 AELOKGERVW FELTOGSITK RSISGTAFGG FLMFKT

SEQ ID NO:2

1 ASSTSLSDLQ SSRTPGVWKA EAEDTSKDPV GRNWCPYPMS KLVTLALCK TEKFLIHSQQ
 61 PCPQGAPDCQ KVVKVMYRMAH KPVYQVKQKV LTS LAWRCGP GYTGPNCCEHH DSMAIPEPAD
 121 PGDSHQEPPQD GPVSFKPGHL AAVINEVEVQ QEQQEHLLGD LQNDVHRVAD SLPGLWKALP
 181 GNLTAASLSN DVKNVGRCC AEAGAGAASL NASLHGLHNA LFATQRSLEQ HQRLFHSLFG
 241 NFQGLMEANV SLDLGKLQTM LSRKGKKQQK DLEAPRKRD KEEAEPVDIR VTGPVPGALG
 301 AALWEAGSPV AFYASFSEGT AALQTVKFNT TYINIGSSYF PEHGYFRAPE RGVYLFAVSV
 361 EFGPGPGTQO LVFGHHRTPV VCTTGQGS GS TATVFAMAELO QKGERVWFEL TOGSITKRSL
 421 SGTAFGGFLM FKT

SEQ ID NO:3

1 EAEPLVDIRV TGPVPGALGA ALWEAGSPVA FYASFSEGA ALQTVKFNTT YINIGSSYFP
 61 EHGYFRAPE RGVYLFAVSVE FGPGPGTQO VFGHHRTPV CTTGQGSGST ATVFAMAELO
 121 KGGERVWFELT OGSITKRSL S GTAFGGFLMF KT

SEQ ID NO:4

TPVCTTGQGS GSTATVFAMA ELQK

SEQ ID NO:5

VWFELTQGSI TK

SEQ ID NO:6

SLSGTAFGGF LMFK

Figure 1b / 3**SEQ ID NO:7**

1 atgatcctgagcttgctgttcagcctggggccccctggctggggctgtggggca
61 tggcccccaggcttccagtactagcctctgtatctgcagagctccaggacacctgggtc
121 tggaaaggcagaggctgaggacaccggcaaggaccccgtaggacgttaactggtgcaccc tac
181 ccaatgtccaagctggtcaccttactagctttgcaaaacagagaaaattcctcatccac
241 tcgcagcagccgtgtccgcagggagctccagactgccagaaagtcaaagtcatgtaccgc
301 atggcccacaagccagtgtaccaggtaagcagaaggctgacccctttggcctggagg
361 tgctgccctggctacacggccccactgcgagcaccacgattccatggcaatccctgag
421 cctgcagatcctgggtacagccaccaggAACCTcaggatggaccaggtagcttcaaacct
481 ggccacccctgtgcagtgtcaatgagggtgagggtgcaacaggaacagcaggaacatctg
541 ctgggagatctccagaatgtatgtgcaccgggtggcagacagcctgcccaggcctgtggaaa
601 gcccgcctgtaacccctcacagctgcacgcctgagcaacgcacgtcaagaatgtcgccgg
661 tgctgcaggccgaggccggggccggggccctccctcaacgcctccctcacggcctc
721 cacaacgcactttcgccactcagcgcagctggagcagcaccagcggctttccacagc
781 ctcttgggaacttccaagggtcatggaaaggcaacgtcagcctggacctgggaagctg
841 cagaccatgctgagcagaaagggaagaaggcagcagaaagacctggaagctccccggaaag
901 agggacaagaaggaaagcggagcccttgggacatacgggtcacagggctgtgccaggt
961 gccttgggcggcgctctgggaggcaggatccctgtggccttatgccagctttca
1021 gaagggacggctgcctgcagacagtgaaggtaacaccacatacatcaacattggcagc
1081 agctacttcctgaacatggctacttccgagccctgagcgtgggtctacctgtttgca
1141 gtgagcgttgaatttggccaggcaggcaccggcagctgggtttggaggtcaccat
1201 cggactccagtctgtaccactggcaggggagtgaaagcacagoaacggtcttgccatg
1261 gctgagctgcagaagggtgagcagttatggttgagttaaacccaggatcaataacaaag
1321 agaaggcctgtcggcactgcattggggcttcctgttgttaagacactga

Figure 2a / 3

10 20 30 40 50 60
 ATGATCCTGAGCTTGCTGTTAGCCTGGGGCCCCCTGGCTGGGGCTGCTGGGGCA
 M I L S L L F S L G G P L G W G L L G A

 70 80 90 100 110 120
 TGGGCCAGGCTTCCAGTACTAGCCTCTCTGATCTGCAGAGCTCCAGGACACCTGGGT
 W A Q A S S T S L S D L Q S S R T P G V

 130 140 150 160 170 180
 TGGAAAGGCAGAGGCTGAGGACACCGGCAAGGACCCCCTAGGACGTAACGGTGCCTAC
 W K A E A E D T G K D P V G R N W C P Y

 190 200 210 220 230 240
 CCAATGTCCAAGCTGGTCACCTTACTAGCTCTTGCAAAACAGAGAAATTCCCTCATCCAC
 P M S K L V T L L A L C K T E K F L I H

 250 260 270 280 290 300
 TCGCAGCAGCCGTGTCGCAGGGAGCTCCAGACTGCCAGAAAGTCAAAGTCATGTACCGC
 S Q Q P C P Q G A P D C Q K V K V M Y R

 310 320 330 340 350 360
 ATGGCCCACAAGCCAGTGTACCGGTCAAGCAGAAGGTGCTGACCTCTTGGCTGGAGG
 M A H K P V Y Q V K Q K V L T S L A W R

 370 380 390 400 410 420
 TGCTGCCCTGGCTACACGGGCCCAACTGCGAGCACACGATTCCATGGCAATCCCTGAG
 C C P G Y T G P N C E H H D S M A I P E

 430 440 450 460 470 480
 CCTGCAGATCCTGGTGACAGCCACCAGGAACCTCAGGATGGACCAAGTCAGCTCAAACCT
 P A D P G D S H Q E P Q D G P V S F K P

 490 500 510 520 530 540
 GGCCACCTTGCTGCACTGATCAATGAGGTTGAGGTGCAACAGGAACAGCAGGAACATCTG
 G H L A A V I N E V E V Q Q E Q Q E H L

 550 560 570 580 590 600
 CTGGGAGATCTCCAGAATGATGTGACCGGGTGGCAGACAGCCTGCCAGGCCTGTGGAAA
 L G D L Q N D V H R V A D S L P G L W K

 610 620 630 640 650 660
 GCCCTGCCCTGGTAACCTCACAGCTGCAAGCCTGAGCAACGACGTCAAGAATGTCGGCGG
 A L P G N L T A A S L S N D V K N V G R

 670 680 690 700 710 720
 TGCTGCGAGGCCGAGGCCGGGGCCGGCCCTCCCTCAACGCCTCCCTCACGGCCTC
 C C E A E A G A G A A S L N A S L H G L

 730 740 750 760 770 780
 CACAACGCACTTCCGCCACTCAGCGCAGCTGGAGCAGCACAGCGGCTCTTCCACAGC
 H N A L F A T Q R S L E Q H Q R L F H S

 790 800 810 820 830 840
 CTCTTTGGGAACTTCCAAGGGCTATGGAAGCCAACGTCAGCCTGGACCTGGGGAAAGCTG
 L F G N F Q G L M E A N V S L D L G K L

 850 860 870 880 890 900
 CAGACCATGCTGAGCAGGAAGGGAAAGAAGCAGCACAGAAAGACCTGGAAGCTCCCCGGAAG
 Q T M L S R K G K K Q Q K D L E A P R K

 910 920 930 940 950 960
 AGGGACAAGAAGGAAGCGGAGGCCCTTGGTGGACATAGGGTACAGGGCTGTGCCAGGT
 R D K K E A E P L V D I R V T G P V P G

Figure 2b / 3

970 980 990 1000 1010 1020
 GCCTTGGCGCGCGCTCTGGGAGGCAGGAATCCCCCTGTGGCCTCTATGCCAGCTTTCA
 A L G A A L W E A G S P V A F Y A S F S

 1030 1040 1050 1060 1070 1080
 GAAGGGACGGCTGCCCTGCAGACAGTGAAGTTAACACACCATAACATCAACATTGGCAGC
 E G T A A L Q T V K F N T T Y I N I G S

 1090 1100 1110 1120 1130 1140
 AGCTACTTCCCTGAACATGGCTACTTCCGAGCCCCCTGAGCGTGGTGTCTACCTGTTGCA
 S Y F P E H G Y F R A P E R G V Y L F A

 1150 1160 1170 1180 1190 1200
 GTGAGCGTTGAATTGGCCCAGGGCCAGGCACCAGGCAGCTGGTGTGGAGGTACCAT
 V S V E F G P G P G T G Q L V F G G H H

 1210 1220 1230 1240 1250 1260
 CGGACTCCAGTCTGTACCACTGGGCAGGGGAGTGGAAAGCACAGCAACGGTCTTGCCATG
 R T P V C T T G Q G S G S T A T V F A M

 1270 1280 1290 1300 1310 1320
 GCTGAGCTGCAGAAGGGTGAGCGAGTATGGTTGAGTTAACCCAGGGATCAATAACAAAG
 A E L Q K G E R V W F E L T Q G S I T K

 1330 1340 1350 1360 1370
 AGAAGCCTGTCGGGCACTGCATTGGGGGCTTCCTGATGTTAACGACCTGA
 R S L S G T A F G G F L M F K T *

Figure 3 / 3

CLUSTAL W (1.81) multiple sequence alignment of SEQ ID NO:1 and Q8K1Z7
(murine homolog)

SEQ ID NO:1	MILSLLFSLGGPLGWGLLGAWAQASSTSLSDLQSSRTPGVWKAEAEDTGKDPVGRNWCPY
Q8K1Z7	MIPTLLLGFGVYLSWGLLGSAQDPGTFSHLNRPGMPEGWRLGAEDTSRDPIRRNWCPY
	** :**:.* *.******:*** ..*.:.*: . * *: * ***.:**: *****
SEQ ID NO:1	PMSKLVTLLALCKTEKFLIHSQQPCPQGAPDCQKVVKVMYRMAHKPVYQVKQKVLTSLAWR
Q8K1Z7	QKSRLVTFVAACKTEKFLVHSQQPCPQGAPDCQGVRVMYRVAQKPVYQVQQKVLISVDWR
	*:***:.* ******:*****:***** *:****:.*:*****:***** *: **
SEQ ID NO:1	CCPGYTGPNCCEHDSMAIPEPADPGDSHQEPQDGPFVSKPGHLAAVINEVEVQQEQQEHL
Q8K1Z7	CCPGFQGPDCQDHNPNTANPEPTEPSPGKLQETWDSDMDGFELGHGPVPEFNEIKVPQEQQE--
	*****: **:.*:.*.. * ***:.*... **. *. ..*: ** .. :**:.* *****
SEQ ID NO:1	LGDLQNDVHRVADSLPGLWKALPGNLTAASLSNDVKNVGRCEAEAGAGAASLNASHGL
Q8K1Z7	-----IRRLSSDVKQIGQCCEASW---AASLNSSLEDL
	.*:.*:****. *****:***..*
SEQ ID NO:1	HNALFATQRSLEQHQRLFHSLFGNFQGLMEANVSDLGKLQTMILSRKGKKQQKDLEAPRK
Q8K1Z7	HSMLLDTQHGLRQHRQLFHNLFQNFQGLVASNISLDLGKLQAMLSKKDKQPRGPGESRK
	*. *: **:.*:.*:*****.** ****: :*:*****:***:*.*** :. .**
SEQ ID NO:1	RDKKEAEPLVDIRVTGPVPGALGAALWEAGSPVAFYASFSEGTAALQTVKFNTTYINIGS
Q8K1Z7	RDKKQVVMSTDAHAKG-----LELWETGSPVAFYAGSSEGATALQMVKFNTTSINVGS
	*****:.. .* :..* ***:*****. ***:*** ***** **:***
SEQ ID NO:1	SYFPEHGYFRAPERGVYLFAVSVEFGPGPGTGQLVFGHHRTPVCTTGQGSSTATVFAM
Q8K1Z7	SYFPEHGYFRAPKRGVYLFAVSITFGPGPGMGQLVFEGHHRVPVYSTEQRGGSTATTFAM
	*****:*****:*****:***** *****. ***:*** ***** **:*** .*****.***
SEQ ID NO:1	AELQKGERVWFELTQGSITKRSLSGTAFGGFLMFKT
Q8K1Z7	VELOKGERAWFELIQGSATKGSQPGTAFGGFLMFKT
	.*****.**** *** ** * .*****